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	extensin homolog T9E8	retinoblastoma protei	NADH dehydrogenase su	secF protein - Strept	nitrate transporter -	hypothetical protein	endocuticular protein	H+-transporting ATP s	cobalamin (5'-phospha	cyclic nucleotide-gat	acrosin (EC 3.4.21,10	NADH dehydrogenase (u	extensin-like protein	cyclase-associated pr	phosphotransferase sv	transactivator EBNA-2	61K protein - Autogra	hypothetical 60.7K pr	conserved hypothetica	probable Na+/H+-excha	eyelid - fruit fly (D	Fî protein - avian in
	T06291	A57640	T13684	S52766	A70320	T00691	S78091	A45612	E69254	A57652	S29599	C22845	T06076	S47091	G64918	A45690	525128	H40781	S55420	S61395	T13049	VFIHB1
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.....VRTAAANAAAGAAENAFRAP 347 Mean 49.533; Variance 128.029; scale 0.387 142080 segs, 47172406 residues pir62 1:pirl 2:pir2 3:pir3 4:pir4 >US-09-360-125-1 (1-347) from US09360125.pep 2538 1 MAQSRDGGNPFAEPSELDNP...... Post-processing: Minimum Match 0% Listing first 45 summaries PAM 150 Gap 11 Title: Description: Perfect Score: Sequence: Scoring table: Statistics: Database: Searched:

protein - protein database search, using Smith-Waterman algorithm

Fri Jun 16 08:49:52 2000;

not generated.

Tabular output

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Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Pred. No.	0.00+000	9.04e-181	1.57e-92	6.05e-12	1.46e-03	3.15e-02	1.09e-01	8.49e-02	7.42e-01	7.42e-01	4.62e-01	7.426-01	7.42e-01	7.42e-01	5.86e-01	4.62e-01	9.39e-01	1.50e+00	1.50e+00	9.39e-01	1.50e+00	1.50e+00	1.50e+00
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241 FDQDVLFVLQAIGIPGWGFSGWISALVVPKGNTAVSVLMLLVALLFTGIAVLĞIVMLKRI 300

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 VHVLQAAGFHNWGNCGWISSLTGLNKNIPVGIMMIIIAALFTASAVISLVMFKKVHGLYR 290
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                                                                                                                  $37395 #type complete
secretory carrier membrane protein 37 - rat
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#formal_name Rattus norvegicus #common_name Norway rat
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
09-5ep-1994
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#formal_name Caenorhabditis elegans
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115.28
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#length 338 #molecular-weight 37998 #checksum 9593
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Pred. No. 9.04e-181;
71; Mismatches 63; Indels 17;
                                                                                                                                                                                                                                                                                                                                            ##molecule_type protein
##residues 53-78,105-116,299-322 ##label BR2
OS calcium binding; leucine zipper; transmembrane
                                                                                                                                                                                                                                                                                             not compared with conceptual translation
                                     291 TTGASFEKAQQEFATGVMSNKTVQTAAANAASTAATSA 328
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                                                                                                                                                                                                            Brand, S.H.; Castle, J.D.
EMBO J. (1993) 12:3753-3761
SCAMP 37, a new marker within the
recycling system.
                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
##residues 1-338 ##label BRA
                                                                                                                                                                                                                                                                  cross-references MUID:94008982
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Best Local Similarity 55.3%;
Matches 187; Conservative
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Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Conway, A.; Kurtz, D.; Ojl, O.; Shen, Y.K.; Toxiumi, M.; Vysotskaha, V.; Yu, G.; Davis, R.W.; Federspiel, N.A.; Theologis, A.; Ecker, J.R. submitted to the EWBL Data Library, January 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 GNTAVSVLMLLVALLETGIAVLGIVM-LKRIHSLYRRTGASFQKAQQEFAAGVFSNPAVR 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 EVEIPVQFQKTVTFAYYVFLMYVLALVVNVLASL-FYMIFAGGSIGQLFLACIQLALFSP 184
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#length 221 #molecular-weight 24765 #checksum 5742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence for Arabidopsis thallana BAC F2187, T00903
                                                                                                                                                                   ##residues___1=324 ##label GAT
##cross-references EMBL.AF003739; NID:g2105487;
##experimental_source strain Bristol N2; clone M01D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues
##residues
##cross-references EMBL:ACO02560; NID:92618677; PID:92809248;
GSPDB:GN0059; ATSP:F21B7.17
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                                                                                    **status preliminary; translated from GB/EMBL/DDBJ
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Gattung, S.; Goela, D.; Wilson, R. submitted to the EMBL Data Library, May The sequence of C. elegans cosmid MOID7.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 748; DB 2; Ler
Pred. No. 1.57e-92;
70; Mismatches 63;
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Best Local Similarity 43.1%;
Matches 110; Conservative
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		27	116	4.8	734 2	T13685	NADH dehydrogenase -	6.51e-01
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Copyright (c) 1993-1998 Universi	ty of Edinburgh, U.K.	38	113	4.6	274 2	S42172	NADH dehydrogenase (u	1.32e+00
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ALIGNMENTS

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>US-09-360-125-3 (1-329) from US09360125.pep 2434 1 MSAFDINPFADPVDVNPFQD......

Title: Description: Perfect Score: Sequence:

Tabular output not generated.

MPsrch_pp

Run on:

142080 seqs, 47172406 residues

PAM 150 Gap 11

Scoring table:

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics:

Database:

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Mean 49.328; Variance 126.753; scale 0.389

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Conway, A.; Kurtz, D.; Oji, O.; Shen, Y.; Torlund, M.; Vysotskala, V.; Yu, G.; Davis, R.W.; Federspiel, N.; Theologis, A.; Ecker, J.R. submitted to the EMBL Data Library, January 1998 Genomic sequence for Arabidopsis thaliana BAC F21B7.
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ITAB_HUMAN
YCYB_LEITA
SBMA_ECOLI
NUJAM_CHOCR
Y390_MYCPN
NUSC_ATHGR
NUSC_ATHGR
NUSC_CATHGR
NUSC_CATCON
NUSC_CATCON

*************	(WE)	3.1A John F. Collins, Biocomputing Research Unit. t (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	protein database search, using Smith-Waterman algorithm	00; MasPar time 14.93 Seconds	o'i.ooi miiion ceii abaaces/sec	5.pep		ssidues	of the state of th		110:051; scale 0.455	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
************************		Release 3.1A John F. Collins, Biocomputing Research Unit Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	MPsrch_pp protein · protein database a	Run on: Fri Jun 16 08:51:14 2000;	Tabular output not generated.	Title: >US-09-360-125-3 Description: (1-329) from US09360125.pep Perfect Score: 2434 Sequence: 1 MSAEDINPFADPVDVNPFQD	Scoring table: PAM 150 Gap 11	Searched: 83857 seqs, 30454973 residues	Post-processing: Minimum Match 0% Listing first 45 summaries	Database: swiss-prot38 1:swissprot	Statistics: Mean 50.077; Variance 110:051;	Pred. No. is the number of results predicted by chance to score greater than or equal to the score of the result being and is derived by analysis of the total score distribution

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				MEDLINE; 98017831. Singleton D.R., Wu T.T., Castle J.D.; "Three mammalian SCAMPS (secretory carrier membrane proteins) are highly related products of distinct genes having similar subcellular	AS A	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profil institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	 	Gaps
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			mma]	otei ar s	WAYS.	ough rest ent an	fam	328
			SCAMPZ. SUKATORIAS (Human). BUKATYOCA, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. [1]	MEDLINE; 98017831. Singleton D.R., Wu T.T., Castle J.D.; Three mammalian Schare (secretory carrier membrane proteins) are highly related products of distinct genes having similar subcellu	ributions."; ell Sci. 110:2099-2107(1997). RUNCIION: FUNCTIONS IN POST-GOLGI RECYCLING PATHWAYS. ACTS AS RECYCLING CARRIER TO THE CELL SURRACE. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. TISSUE SPECTFICITY: WIDELY EXPRESSED.	roduced through its and the En re are no resti as its content . Usage by an. http://www.isb-s	EMBL; AF005038; AAB62723.1; Transmembrane; Transport; Protein transport; Multigene family. TRANSMEM 153 173 POTEWTIAL. TRANSMEM 218 231 POTEWTIAL. TRANSMEM 218 238 POTEWTIAL. TRANSMEM 262 282 POTEWTIAL. SEQUENCE 328 AA; 36606 MW; 03015190B7940600 CRC64;	Length 328; Indels
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		S CR	ns () Meta Prima	8017 D.R. malia	ODS. 1. 1. ON: 1 ING (LULA) SPEC	- PROT	5038; 5038; 153 181 218 262 328	m11a;
	SCA2_HUMAN	OLDIA, 1976 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last sequence update) SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN	SCAMFZ. Homo Sapiens (Human) Eukaryota, Metazoa, Eutheria, Primates; [1]	MEDLINE: 98017831. Singleton D.R., Wu T.T., "Three mammalian SCAMPS highly related products of	distributions."; J. Cell Sci. 110:2099-2107(1997)	This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinformathe European Bioinformatics Institute. The use by non-profil institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-slb.ch).	EMBL; AF005038; AAB62723.1; Transmembrane; Transport; Pi TRANSMEM 153 173 TRANSMEM 181 201 TRANSMEM 218 238 TRANSMEM 262 282 SEQUENCE 328 AA; 36606 MF	ch 1 Simi. 327;
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SUMMARIES

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                        120 PPLPSWCPVKPCFYQDFSTEIPADYQRICKMLYYLWMLHSVTLFLNLLACLAWFSGNSSK 179
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83; Mismatches 63; Indels 7; Gaps
                                                                                                                                                                                            GLGDSGWIAALSTLDNHSLAISVIMMVVAGFFTLCAVLSVFLLQRVHSLYRRTGASFQQA
MSAFDINPFADPVDVNPFQDPSVTQLINAPQGGLAEFNPFSETNAATIVPVTQLPGSSQP
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Rattus.
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                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SEGRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1 (SCAMP 37).
SCAMPI OR SCAMPI
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72E3BAD6A8FEBF59 CRC64;
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-!- FUNCTION: FUNCTIONS IN POST-GOLG! RECYCLING PATHY
ENCYCLING CARRIER TO THE CELL SURFACE.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-!- SIMILARITY: BELONGS TO THE SCAMP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                     338 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
MEDLINE; 94008982.
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Conservative
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338 AA;
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Matches 175; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mao M., Fu G., Mu J.-S., Zhang Q.-H., Zhou J., Kan L.-X., Huang Q.-H., He K.-L., Gu B.-W., Han Z.-G., Shen Y., Gu J., Yu Y.-P., Xu S.-H., Hang Y.-L., Gu B.-W., Han Z.-G., Shen Y., Gu J., Yu Y.-P., Xu S.-H., Mang Y.-L., Gu B.-W., Han Z.-G., Shen Y., Gu J., Yu Y.-P., Xu S.-H., Indentification of genes expressed in human CD34(+) hematopoietic stem/progenitor cells by expressed sequence tags and efficient full-length cDNa cloning.", J. S. 95:8175-8180(1998).

-I-FUNCTION: FUNCTIONS IN POST-GOLGI RECYCLING PATHWAYS. ACTS AS A RECYCLING CARRIER TO THE CELL SURFACE.

-I-SUBCELLULAR LOCATION: INTEGRAL EMBERANCE.

-I-SUBCELLULAR LOCATION: INTEGRAL EMBERANCE.

-I-TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN
                                                                                                                                    59 QPAVLQPSVEPTQPTPQAVVSA-AQAGLLRQQEELDRKAAELERKERELQNTVANLHVRQ 117
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                                                         NNWPPLPSNFPVGPCFYQDFSVDIPVEFQKTVKLMYYLWMFHAVTLFLNIFGCLAWFCVD
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Eutheria; Primates; Catarrhini; Hominidae; Homo
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN SCAMP1 OR SCAMP.
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MEDLINE; 98017831.
Singleton D.R., Wu T.T., Castle J.D.;
"Three mammalian SCAMPs (secretory carrier membrane proteins) are highly related products of distinct genes having similar subcellular distributions.";
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-!- FUNCTION: FUNCTIONS IN POST-GOLGI RECYCLING PATHWAYS. ACTS.
RECYCLING CARRIER 10 THE CELL SURFACE.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SUBCELLULAR: BELONGS TO THE SCAMP FAMILY.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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PROTEIN 3.
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Pred. No. 0.00e+00;
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SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTE
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Best Local Similarity 98.6%;
Matches 342; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               238
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                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                              61 -- LPPPSAPSLQPSRKLSPTEPKNYGSYSTQASAAATAELLKKQEELNRKAEELDRRER
                                                                                                                                                                                                                                                                                                                                                                                                                                       241 IFFVQDVFFVLQAIGIPGWGFSGWVTALVVVGSKPAVAVLMLLDALLFTGIAVLGIVMLK
                                                                                                                                                                                    1 MAQSRDIGNPSPDSGELDNPFQDPAVIQHRPSQQYATLDVYNPFENREPPPAYEPPAPAP
                                                                                                                                                                                                     61 APLPPPSAPSVQSSRKLSPTEPRNYGSYSTQASAAATAELLKKOEELNRTAEELDRRER
                                                                                                                                                                                                                                                                                                      121 ELQHVALGGAGTRQNNWPPLPSFCPVKPCFFQDISMEIPQEFQKTVSTMYYLWMCSTLAL
                                                                                                                                                                                                                                                                                                                                                                181 LINFFACLARFCVDTGSGSGFGLSMLWLLLFTPCSFVCWYRPMYKAFRSDSSFNFFVFFF
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 94008982.
Brand S.H., Castle J.D.;
"SCAMP 37, a new marker within the general cell surface recycling system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 12:3753-3761(1993).
-1- FUNCTION: FUNCTIONS IN POST-GOLGI RECYCLING PATHWAYS. ACTS.
RECYCLING CARRIER TO THE CELL SURFACE.
-1- SUBCELLULAR LOCATION: INTEGRAL WEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE SCAMP FAMILY.
EMBL; AF005036; AAB62721.1; -.
Transmembrane; Transport; Protein transport; Multigene family.
                                                                                                                                                          .;
7
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Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transport; Protein transport; Multigene family
                                                                                                                            Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1 (SCAMP 37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2321; DB 1; Length 34 Pred. No. 0.00e+00; 23; Mismatches 12; Indels
                                                                                               D54A514769A49309 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
                                                     POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L22079; -; NOT_ANNOTATED_CDS.
                                                                                               38387 MW;
                                                                                                                            Match 91.4%;
Local Similarity 89.4%;
les 312; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                     . 220
256
297
                                                                                               349 AA;
                                       169
200
236
277
                     Transmembrane;
TRANSMEM 169
TRANSMEM 200
TRANSMEM 236
TRANSMEM 2736
SEQUENCE 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCAMP1 OR SCAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
TRANSMEM 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCA1_RAT
P56603;
                                                                                                                            Query Match
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